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Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE TO CLAIMS

3. (Amended) A [protein] polypeptide comprising an amino acid sequence which is at least 60 % homologous to the amino acid sequence of SEQ ID NO: 1, and having transaldolase activity.

4. (Amended) A DNA coding for the polypeptide of any one of claims 1 to 3, or the DNA of SEQ ID NO: 2.

6. (Amended) A DNA which hybridizes with the DNA of claim 4 [or 5] under stringent conditions, and codes for a polypeptide having transaldolase activity.

7. (Amended) A recombinant DNA obtain[able]ed by ligating the DNA of [any one of] claim[s] 4 [to 6] with a vector.

9. (Amended) A transformant in which one or more nucleotides have been substituted, deleted or inserted in the nucleotide sequence of the DNA of [any one of claims 4 to 6] carried by the transformant of claim 8 or in the nucleotide sequence of a DNA existing upstream the DNA and participating in transcription and translation, and of which the transaldolase activity is enhanced over that of the transformant not having undergone the substitution, deletion or insertion.

10. (Amended) The transformant according to claim 8 [or 9], wherein the transformant has an ability to produce an aromatic amino acid or aromatic vitamin.

12. (Amended) A transformant in which one or more nucleotides have been substituted, deleted or inserted in the nucleotide sequence of the DNA [of any one of claims 4 to 6] carried by the transformant of claim 8 or in the nucleotide sequence of a DNA existing upstream the DNA and participating in transcription and translation, and of which the transaldolase activity is lowered below that of the transformant not having undergone the substitution, deletion or insertion, or of which the transaldolase activity is lost.

13. (Amended) The transformant according to claim 8 [or 12], wherein the transformant has an ability to produce a substance selected from L-histidine, riboflavin, nucleic acids and nucleic acid-associated substances.

15. (Amended) A process for producing [the] a polypeptide [of any one of claims 1 to 3], which comprises culturing the transformant of claim 8 in a medium to thereby produce and accumulate the polypeptide [of any one of claims 1 to 3] in the culture, and recovering the polypeptide from the culture.

16. (Amended) A process for producing a saccharide having the dihydroxyacetone moiety of the ketose transferred into the aldose, which comprises allowing a ketose and an aldose to exist in an aqueous medium to coexist with an enzyme source selected from cells of the transformant of claim [8 or] 9, a culture of the

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transformant or a processed product of the culture, to thereby produce and accumulate the saccharide in the aqueous medium, and recovering the saccharide from the aqueous medium.

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VERSION WITH MARKINGS TO SHOW CHANGES MADE TO SPECIFICATION

The paragraph at page 3, lines 17-19 have been amended as follows:

(3) A **[protein] polypeptide** comprising an amino acid sequence which is at least 60% homologous to the amino acid sequence of SEQ ID NO: 1, and having transaldolase activity.

The paragraph starting at page 13, line 15 and ending at page 14, line 7 has been amended as follows:

The host cells include microorganisms belonging to the genus Escherichia, Serratia, Bacillus, Brevibacterium, Corynebacterium, Microbacterium or Pseudomonas, including, for example, Escherichia coli XL1-Blue, Escherichia coli XL2-Blue, Escherichia coli DH1, Escherichia coli MC1000, Escherichia coli KY3276, Escherichia coli W1485, Escherichia coli JM109, Escherichia coli HB101, Escherichia coli No. 49, Escherichia coli W3110, Escherichia coli NY49, Escherichia coli GI698, Escherichia coli TB1, Serratia ficaria, Serratia fonticola, Serratia liquefaciens, Serratia marcescens, Bacillus subtilis, Bacillus [amyloliquefacines] amyloliquefaciens, Brevibacterium ammoniagenes, Brevibacterium immariophilum ATCC 14068, Brevibacterium saccharolyticum ATCC 14066, Brevibacterium flavum ATCC 14067, Brevibacterium lactofermentum ATCC 13869, Corynebacterium glutamicum ATCC 13032, Corynebacterium glutamicum ATCC 13869, Corynebacterium acetoacidophilum ATCC 13870, Microbacterium ammoniaphilum ATCC 15354, Pseudomonas putida and Pseudomonas sp. D-0110.